

FIG.1

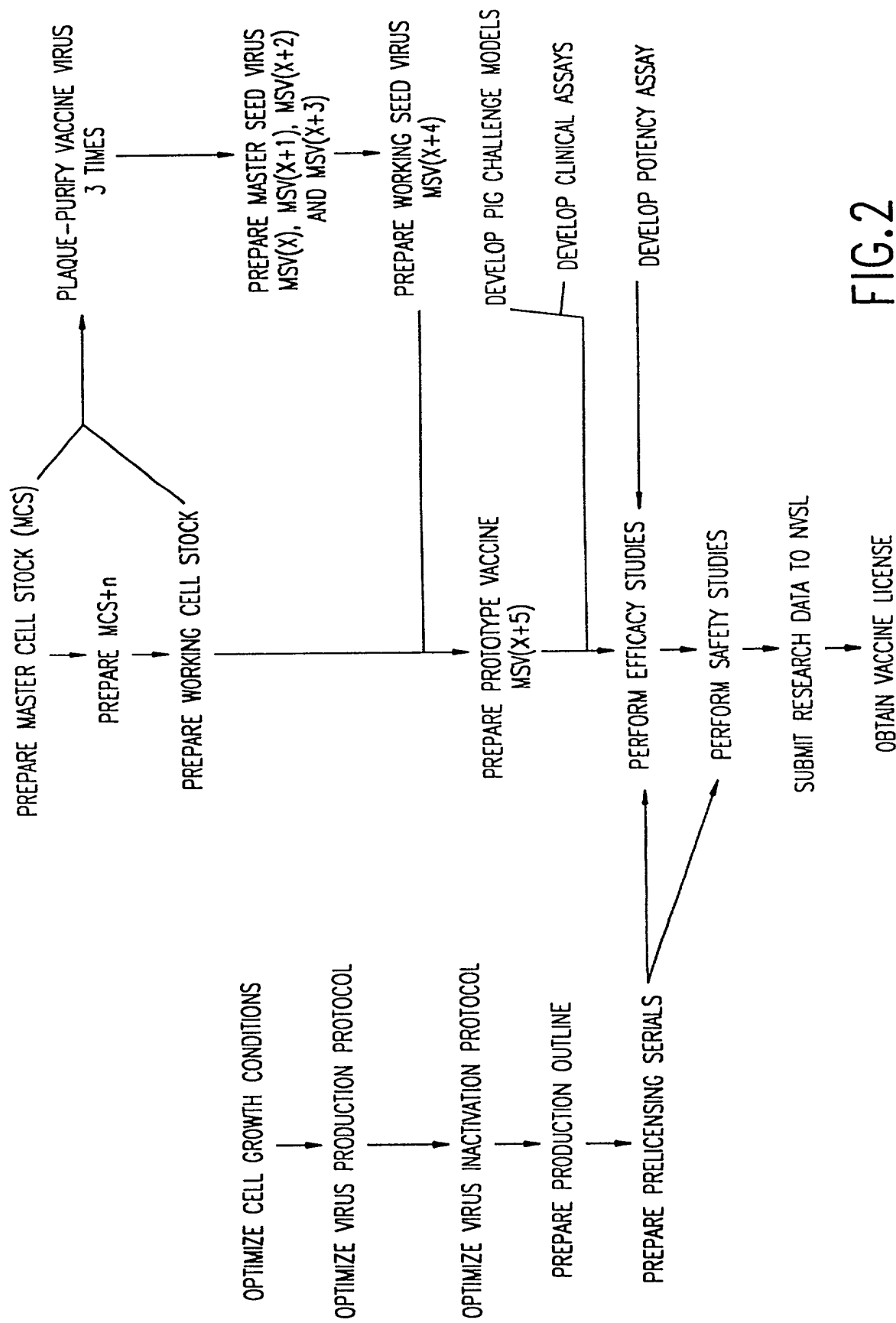


FIG.2

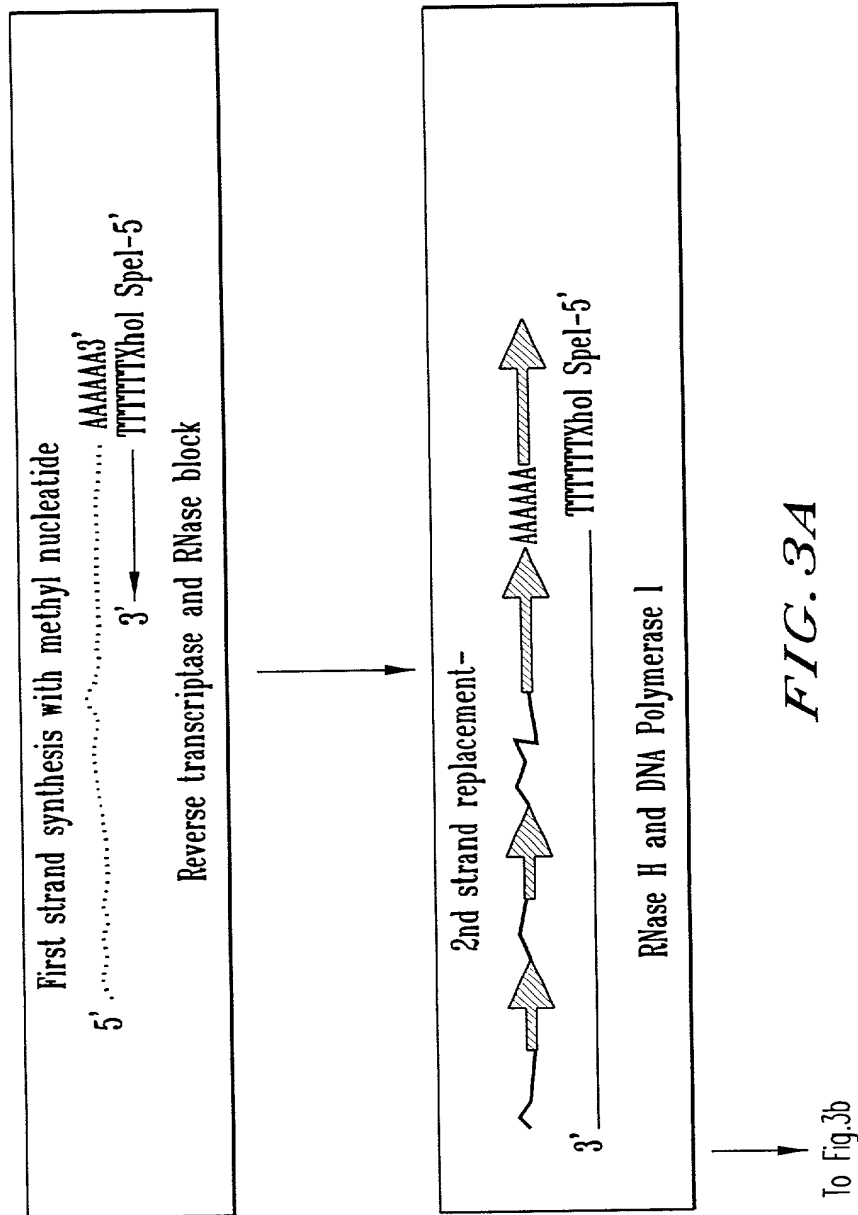


FIG. 3A

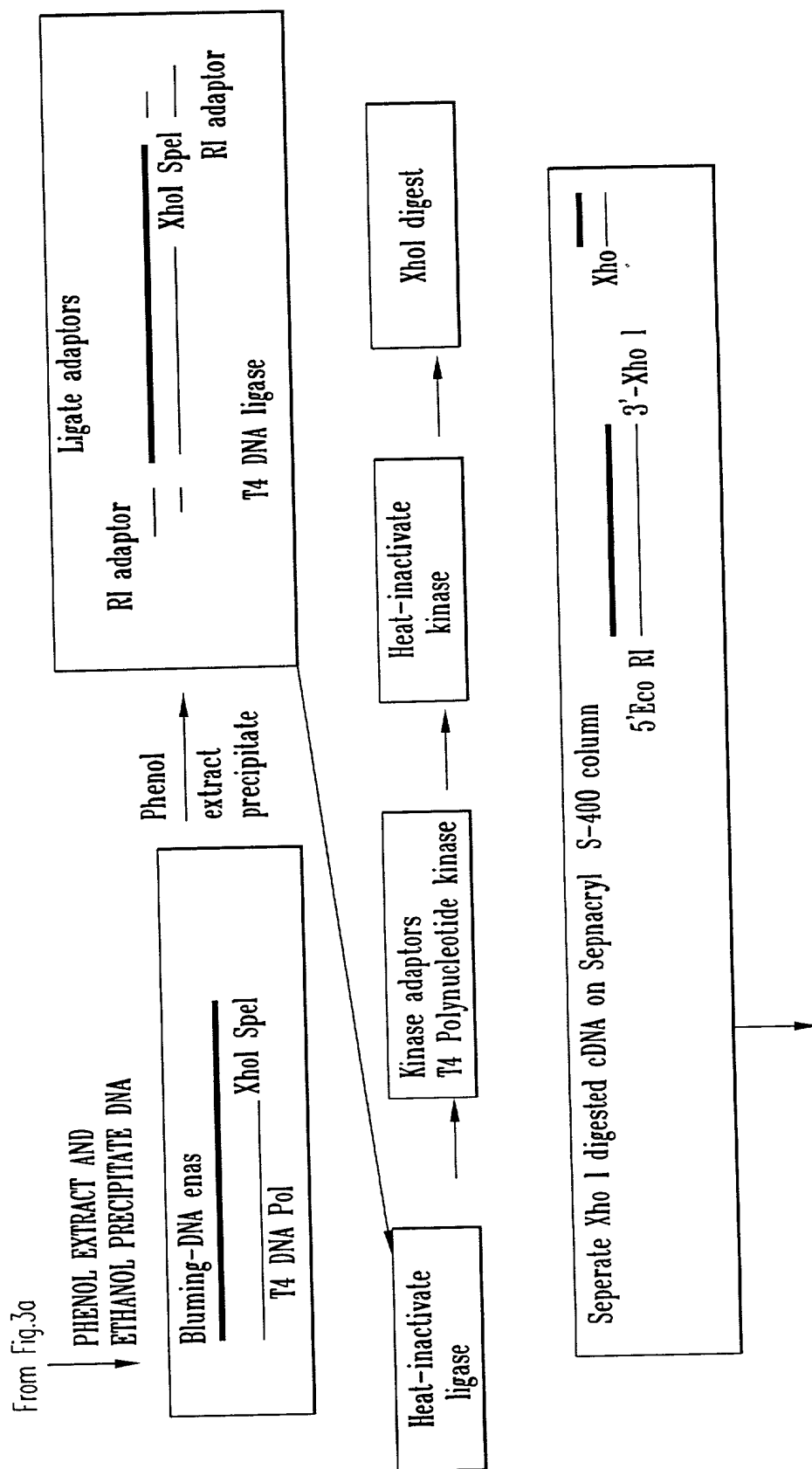


FIG. 3B

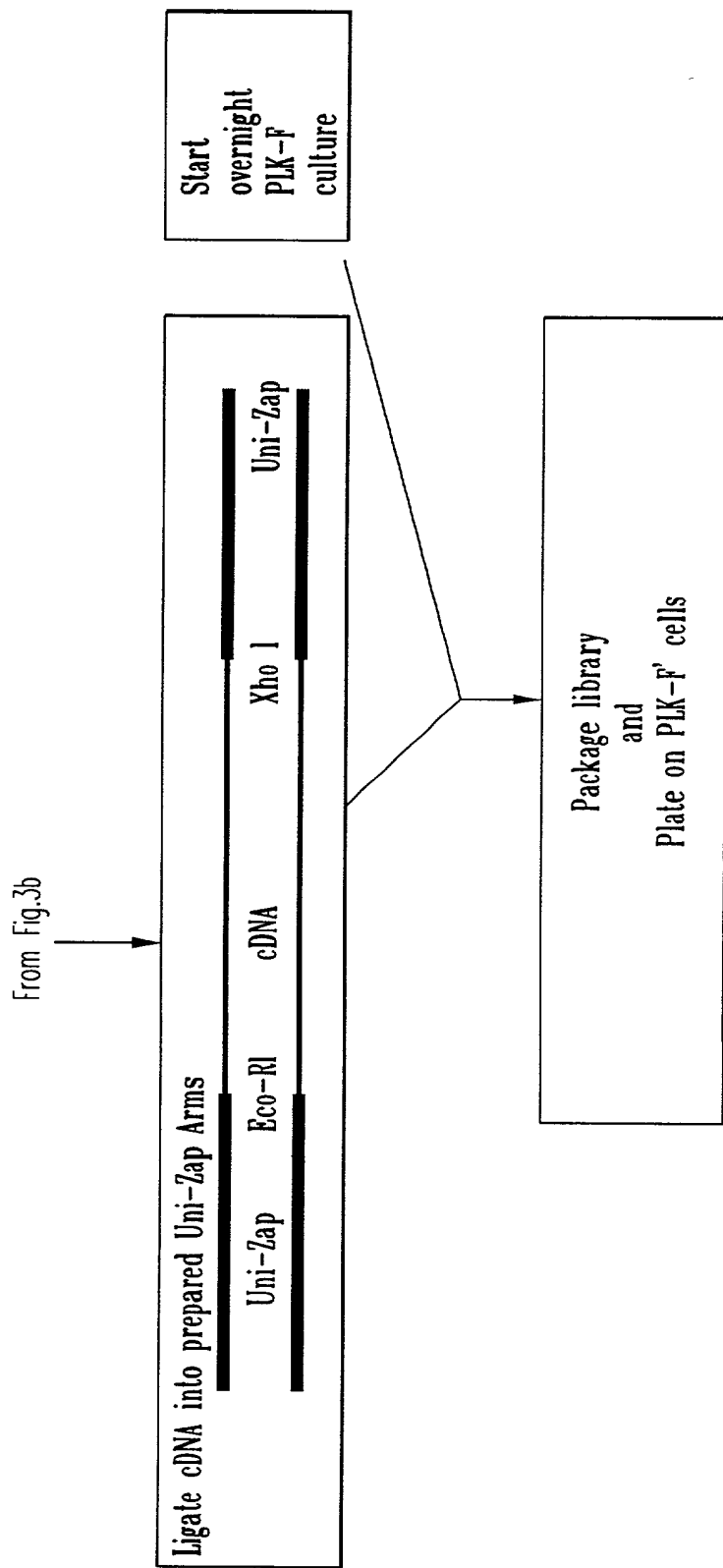


FIG. 3c

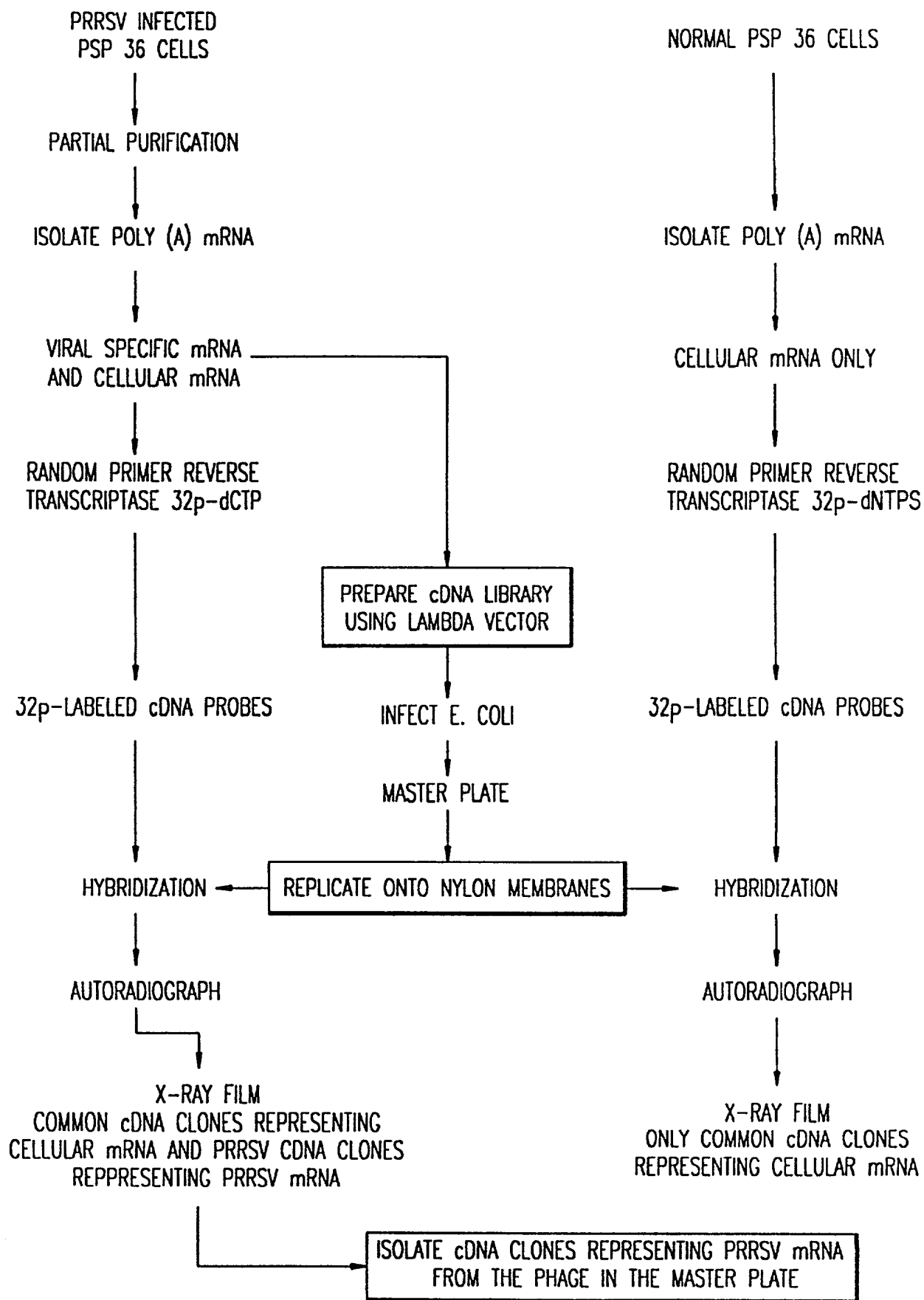


FIG.4

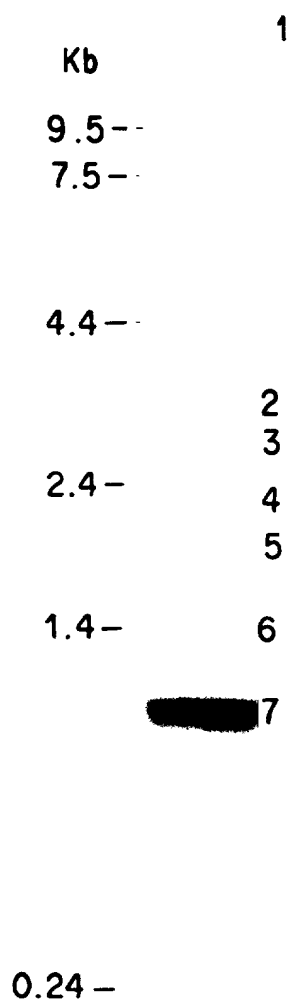


FIG.5

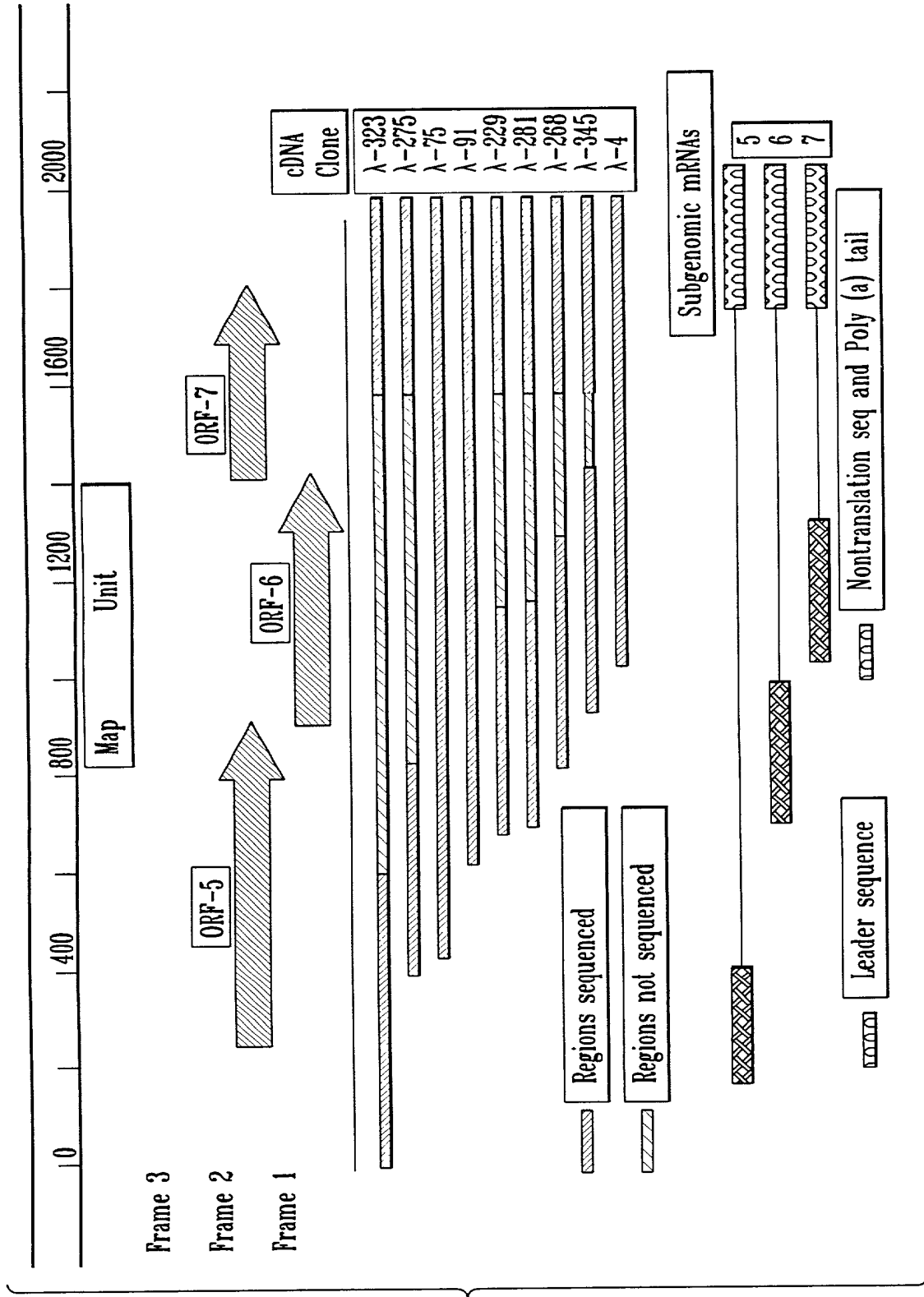


FIG. 6

GGCAGGCTTGGTGTCTCCAAAGACATCAGTTGCCTTAGGCATCGCAACTCGGCCCTCGAGGCGATTGCGAAGTCCCCTCAGTGC CGCACGGCGGATAGGG 100

ACACCGGTGATATCACTGTCACAGCCAAATGTTACCGATGAGAAATTATTGGCATTCCTCTGATCTTCTCATGCTTCTTCTTGCCCTTTTCTATGCTCTG 200

AGATGAGTGAAGAAGGGATTAAAGGTGGTATTTGGCAATGTCAGGCATCGTGGCAGTGGCGTCAACTTACCAGTTACGTCCAACATGTC AAGGAATT 300

TACCCAACGTTCCCTGGTAGTTGACCATGTGCGGTGCTCCATTTCATGACGCCGAGACCATGAGGTGGGCAACTGTTTTAGCCTGTCTTTTGGCATT 400

DRF4 stop
*** +1>DRF5 start

CTGTTGGCAATTTGAATGTTAAGTAIGTTGGGGAAATGCTTGACCGGGGCTGTGCTCGCAATTGCTTTTTTGGGTGATCGTGGCGTCTTGTTTT 500

GTTGGCTCGTCAGCGCCACAGGGACAGCGGCTCAAATTTACAGCTGATTTACAACTTGACGCTATGTAGCTGAATGGCACAGATTGGCTAGCTAATA 600

AATTGACTGGCAGTGGAGTGTTTGTGATTTTCCGTGTTGACTCACATTGCTCTTATGGTGGCCCTCCTACTACTAGCCATTCCCTTGACACAGTCGG 700

TCGTGCTACTGTGCTACCGCTGGGTTTGTTCACGGGGGTAIGTTCTGAGTAGCATGTACGGCGTCTGTGCCCTGGCTGGCTTGATTGCTTCGTCAATT 800

AGGCTTGCGAAGAAATTGCATGTCTCTGGGCTACTCATGTACCAGATATACCAACTTCTTCTGGACACTAAGGGCAGACTCTATCTGTTGGCGGTGGCTG 900

TCATCATAGAGAAAAGGGCAAGTTGAGGTGGAAGGTCACCTGATCGACCTCAAAAGAGTTGTGCTTGATGGTTCGGCGGTACCCCTGT AACCAGAGT 1000

DRF6 start
+1> ***DRF5 stop

TTCAGCGGAACAAATGGAGTCGTCTTAGATGACTTCTGTGTCATGATAGCAGGGCTCCACAAAGGTGCTCTTGGCGTTTTCTATTACCTACACGCCAGTGA 1100

FIG. 7A

TGATATATGCCCTAAAGGTAGTCGGCGCGGCGACTGCTAGGGCTTCGACCTTTTGGCTTCCTGAAATGTTGCTTTCACCTTCGGGTACATGACATTCGT 1200
 GCACCTTCAGAGTACAAATAAGGTGCGGCTCAGTATGGAGCAGTAGTTGCACTCCCTTTGGGGGGTGTACTCAGCCATAGAAACCTGGAAATTCATCACC 1300
 TCCAGATGCCGTTTGTGCTTGCTAGGCGCGCAAGTACATTCTGGCCCCCTGCCACCACGTTGAAAGTGC CGCAGGCTTTCATCCGATTGCGGCAATGATA 1400
 ACCACGCATTTGTGCTCCGGGCTCCACTACGGTCAACGGGCACATTGGTGGCCCGGGTTAAAAAGCCTCGTGTTGGGTGGCAGAAAAGCTGTAA 1500
 ACCAGGGAGTGGTAAACCTTGTAAATATGCCAAATAACACCGGCAAGCAGAGAGAGAGAAAGAGGGGATGGCCAGGCCAGTCAATCAGCTGTGCCAGAT 1600
 GCTGGGTAAAGTATCGCTACCAAAACCAGTCCAGAGGGCAAGGGACCGGGAAGAAAAAATAAGAGAAAAACCCGGAGAGCCCCCATTTCCCTCTAGCG 1700
 ACTGAAGATGATGTCAGACATCATTACCCCTAGTGAGGTCATTTGTGCTGTGTCATCCAGACCGCCTTTAATCAAGGGCGCTGGGACTTGCACCC 1800
 TGTACAGATTCAGGGAGGATAAGTTACACTGTGGAGTTAGTTTGCTACGCATCATACTGTGGCCCTGATCCGGGTCACAGCATCACCCTCAGCATGATG 1900
 GGC TGGCATTC TTGAGGCATCC CAGTGT TGAATTGGGAAGAAATGCGTGGTGAATGGCAGCTGATTGACATTGTGCCCTCTAAGTCACCTATTCAATTAGGGC 2000
 GACCGTGTGGGGTAAGATTTAATTGGCGAGAACACACAGCGCCGAAATTAATAAAAAAAAAAAAA 2062

DRF7 start
 +1> ***DRF6 stop

***DRF7 stop

FIG. 7B

LELYSTAD SEQ (13484-14089)	ATGAGATGTTCTCACA	AAATGGGGCGTTCTTGACTCCGCAC	TCTTGGCTCTGGGTTGGCTTTTTTTC	TGCTGGTA--	13556
ISU-12-3' TERMINAL (426-1028)	-----	ATGTTGGGAAATCTTGACCGCGGCT	TGTGCTCGCAATTTGCTTTTTTGT	TGCTGGTATC	485
LELYSTAD SEQ (13484-14089)	----	CCGCTTGTCCTGGT-DCTTTGGGAT	CGCAACGGACAGCTCGACATACCAATA-D	ATATATAA	13624
ISU-12-3' TERMINAL (426-1028)		GTGCGCTCTTGTTTGCTGCTGAGCG	CAACGGACAGCGGCTCAAA	TTACAGCTGATTTACAACTTG	560
LELYSTAD SEQ (13484-14089)	ACGATATCGGAGCTGAA	TGGACCGACTGGTTGTCCAGCCATTTTGG	TGGGCAGTGGAGACCTTTGT	TGCTTTAC	13699
ISU-12-3' TERMINAL (426-1028)	ACGCTATGTGAGCTGAA	TGGACAGATTTGGCTAGCTAATAATTTGAC	TGGGCAGTGGAGTGTTTTG	CAATTTT	635
LELYSTAD SEQ (13484-14089)	CCGGTTGCCACTCATATCC	CTCTACCTGGTTTCTCACACACAGCCATTTT	TGACCGGCTCGGCTCTGGG	CGCT	13774
ISU-12-3' TERMINAL (426-1028)	CGTGTGTTGACTCAGAT	TGCTGTATGGTGCCCTCAC	TAGCCATTTCCCTTGACACAG	TCGGCTCTGGTCACT	710
LELYSTAD SEQ (13484-14089)	GATCCACTGCAAGATTGTT	GGCGGGGGTACGTACTCTGCAGCGTCTAC	GGCGCTTGTCGTTTGCGAGCGGTTC		13849
ISU-12-3' TERMINAL (426-1028)	GTGCTACCGCTGGGTTGTT	GCAGGGGGTATGTTCTGAGTAGCATGTAC	CGGCTGTGCGCTGGCTGGCTTG		785
LELYSTAD SEQ (13484-14089)	GATGTGTTTGTCATCCGT	GCTAAAAATTGGCATGGCTTCCCGGTAT	GCCGTACCGGTTTACCAACTTCATTT		13924
ISU-12-3' TERMINAL (426-1028)	AATTTGCTTCGTCAATAG	CTTGGCAAAATTGGCATGTCTTCCGCTACT	CTATGTACCAATATACCAACTTTCTTT		860
LELYSTAD SEQ (13484-14089)	GTGGACGACCGGGGAGAGTT	CATCGATGGAGTCTCCAAATAGTTGG	TAGAAAAATTTGGGCAAAAGCCGAGTCCGAT		13999
ISU-12-3' TERMINAL (426-1028)	CTGGACACTAAGGGGAGACT	CTATCGTTGGCTTCCCTGCTCCCTGATCAT	TAGAAAAAGGGGCAAAAGTTGAGGTCGAA		935
LELYSTAD SEQ (13484-14089)	GGCAACCTCGTCAACCAT	CAAAACATGTGCTCCGAAAGGGTTAAAGCT	CAACCCCTTGACAGGAGCTTGCGTGA		14073
ISU-12-3' TERMINAL (426-1028)	GGTCACCTGATCGACCT	CAAAAGAGTTGTCTTGATGGTTCCGCGGCT	TACCCCTGTAAACAGAGTTTCAAGCGGA		1009
LELYSTAD SEQ (13484-14089)	GCAATGGGAGCCCTAG-----				14089
ISU-12-3' TERMINAL (426-1028)	ACAAATGGAGTGGTCCCTTAG				1028

FIG. 8

ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	AATGGAGTGG TCGTACATG ACTTGTGTCAT TGATAGACCG GGTCCACAAA AGGTGCTCTT -ATGG-CAGG --CGTAGACG ATTCTGCAA CGATCCATATC GCGGCACAAA AGCTGGTGGT	947 14132
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	GGGTTTCT ATTAACATACA CCGCAGTATGAT GATATATGCC CTAAAGGTGA GTCCGGGGCG ACCGTTTACC ATCACAATACA CACCTATTAAT GATATACGCC CTAAAGGTGT CACGGGGCGG	1007 14192
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	ACTGCTAGGG CTCTGCACC TTTTGGTCTT CCTGAAATGT GCTTCACTT TCGGGTACAT ACTCTCGGG CAGTTCACCA TCCTAATATTT TCTGAACATGT TCGTATACAT TCGGATACAT	1067 14252
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	GACATTCGTG CACTTTCAGA GTACAAATAA GTTCGGGCTC ACTATGGGAG CAGTAGTTGC GACATATCTG CATTTTCAAT CCACCAACCG TGTCCGACTT ACCCTGGGGG CTGTTGTCG-	1127 14311
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	ACTCTTTTGG GGGGTGTACT CAGC -CATTA GAACCTTGA ATTTATACAC CTCCAGATGC -CCCTTCTGT GGGGTGTCTTA CAGCTTCACA GAGTCAATGGA AGTTTATACAC TTCCAGATGC	1185 14370
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	CGTTTGTGCT TGTACGCCCG CAAGTACATT CTGGCCCCCTG CCCACACAGT TGAAGTGGC AGATTGTGTT GCCTTGGCCG GCGATACATT CTGGCCCCCTG CCCATCACGT ACAAGTGGT	1245 14430
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	GCAGGCTTTT C ATCCGATTGC GGCATAATGAT AACCAAGCAT TTGTGTGTCGG GCGTCCGGGC GCAGGCTCTCC ATTATATCTC AGCGTCTGCT AACCGAGCAT AGCGTGTAG AAAGCCCCGA	1305 14490
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	TCCACTAGCG TCAACGGCAC ATTGGTCCCG GGGTTAAAAA GCCTCGTGT GTGGTGGCACA CTACACTCAG TCAACGGCAC TGTAGTACCA GGAATTCGGA GCCTCGTGT GTGGTGGCANA	1365 14550
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	AAMGCTGTTA AACAGGAGT GGTAAACCTTT GTTAATATG CCAAAATAA CCAGCTGTTA AACAGGAGT GGTAAACCTTC GTTAAGTATG GCGGTAA	1413 14598

FIG.9

Lelystad seq (14588 – 14974)	ATGGCCGGTA AAAACCAAG- GCCAAGAAAGT A-CAG-----C 14632
ISU 12/7a/3' terminal (1403 – 1774)	-----AT GCCAATATAC ACCGGCAAGC AGCAGAAGAG 1434
Lelystad seq (14588 – 14974)	TCCGATGGGG AATGGCCAGC CAGTCAATCA ACTGTGCCAG TTGCTGGGTG 14681
ISU 12/7a/3' terminal (1403 – 1774)	AAAGAGCGGG CATGGCCAGC CAGTCAATCA GCTGTGCCAG ATGCTGGGT- 1483
Lelystad seq (14588 – 14974)	CAATGATATA GTCCACAGCC CACCAAGCTA GCGG--A-GG ACAGGCCAAG 14728
ISU 12/7a/3' terminal (1403 – 1774)	-AA-GATCAT CGCTACAGAA AACAGTCCA GAGGCAAGGG ACCGG---GA 1528
Lelystad seq (14588 – 14974)	AAGAAAAA-- ----G----- -CCTGAGAAG CACATTITTC CCGTGGGTGG 14766
ISU 12/7a/3' terminal (1403 – 1774)	AAGAAAAATA AGAAGAAAAA CCGCGAGAAG CCGCATTTCC CTCIAGCGAG 1578
Lelystad seq (14588 – 14974)	TGAAGATGAC ATCCGGGACC ACCTACCCCA GACTGAAGCG TCCGTCTGCT 14816
ISU 12/7a/3' terminal (1403 – 1774)	TGAAGATGAT GTACAGATTC ACTTTACCCC TAGTACCGGT CAAATTGTGTC 1628
Lelystad seq (14588 – 14974)	TCCAATTCAT CCAGACCGGT TTCAATCAAG GCGCAGGAAG -TGGCTGGCT 14865
ISU 12/7a/3' terminal (1403 – 1774)	TGTGTTAAT CCAGACCGCC TTTAATCAAG GCGCTGGGAG TTGCAAG-CI 1677
Lelystad seq (14588 – 14974)	TTTCATCCAGC GGAAGGTCA GTTTTCAGGT TGAGTTTATG CTGCGCGTTG 14915
ISU 12/7a/3' terminal (1403 – 1774)	GTCAGATTCA GGGAGGATTA GTTACACTGT GGAGTTTATG TTGCGTACGC 1727
Lelystad seq (14588 – 14974)	CTCATAACAGT GCGCCCTGATTT CCGGTGAGTT CTACATCCGC CAGTACAGGT 14965
ISU 12/7a/3' terminal (1403 – 1774)	ATCATACTGT GCGCCCTGATC CCGGTGACAG CATCACCG-T CAG-CATGA- 1774
Lelystad seq (14588 – 14974)	GCAAGTTAA 14974
ISU 12/7a/3' terminal (1403 – 1774)	1774

FIG.10

ISU 12/7a/3' terminal (1775 – 1938)	TGGGCTGGCA TTCTTGAGGC ATCCACTGT TTGAATTGGA	1814
Lelystad seq (14975 – 15101)	-----	14976
ISU 12/7a/3' terminal (1775 – 1938)	ACAAATGGCTG GTGAATGGCA CTGATTGACA TTGTCCTCT	1854
Lelystad seq (14975 – 15101)	TGACAGTCAG GTGAATGGCC GCGATTGGCG TTGTCCTCT	15016
ISU 12/7a/3' terminal (1775 – 1938)	AAGTCACCTA TTCAATTAGG GCGACCTGT GGGGTACGA	1800
Lelystad seq (14975 – 15101)	GAGTCACCTA TTCAATTAGG GCGATACAT GGGGTACATA	15056
ISU 12/7a/3' terminal (1775 – 1938)	TTTAAATT-GG GAGAACCAAC ACCTCCGAAA TTAAAAAAA	1933
Lelystad seq (14975 – 15101)	CTTAAATCAGG CAGCAACCAT GTTACCGAAA TTAAAAAAA	15096
ISU 12/7a/3' terminal (1775 – 1938)	AAAAA	1938
Lelystad seq (14975 – 15101)	AAAAA	15101

FIG. 11

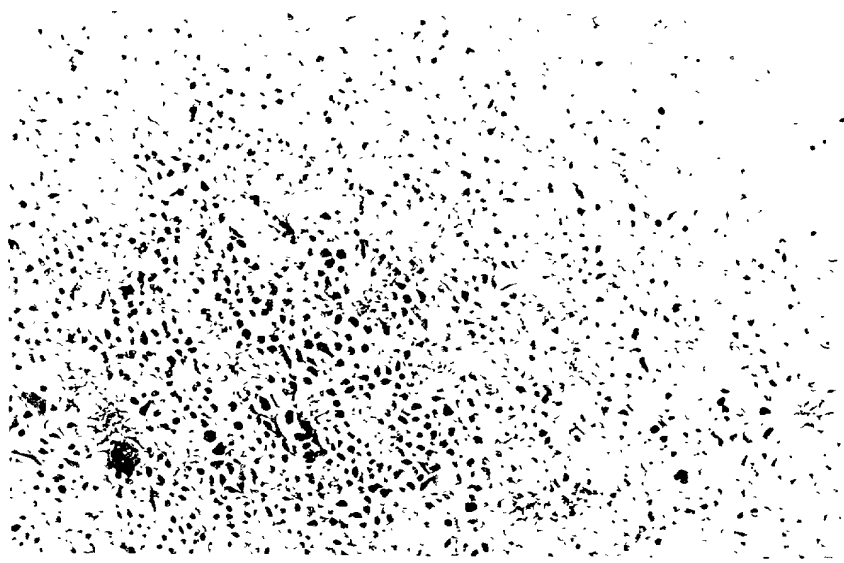


FIG.12

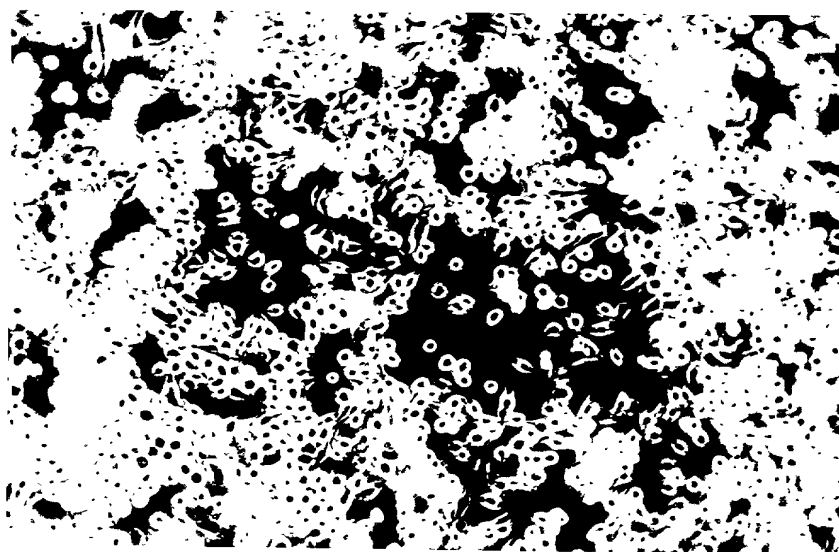


FIG.13

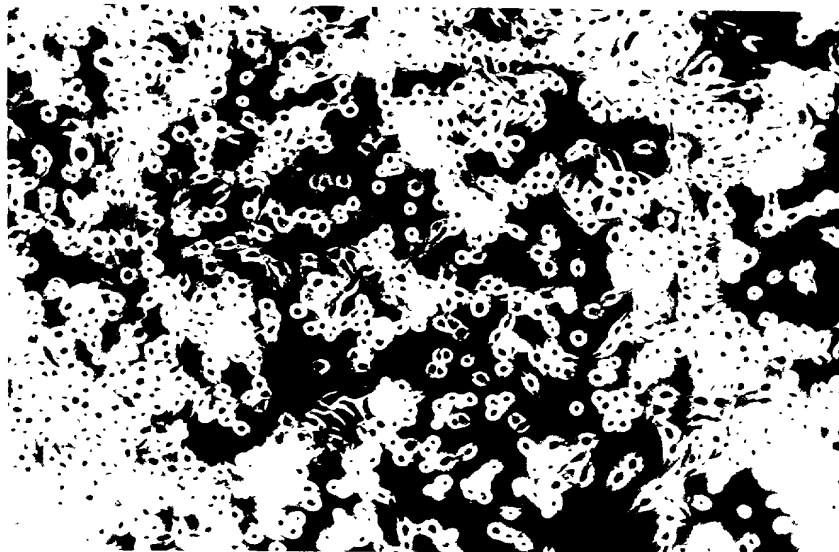


FIG.14

SM E M NP E+M+NP SM

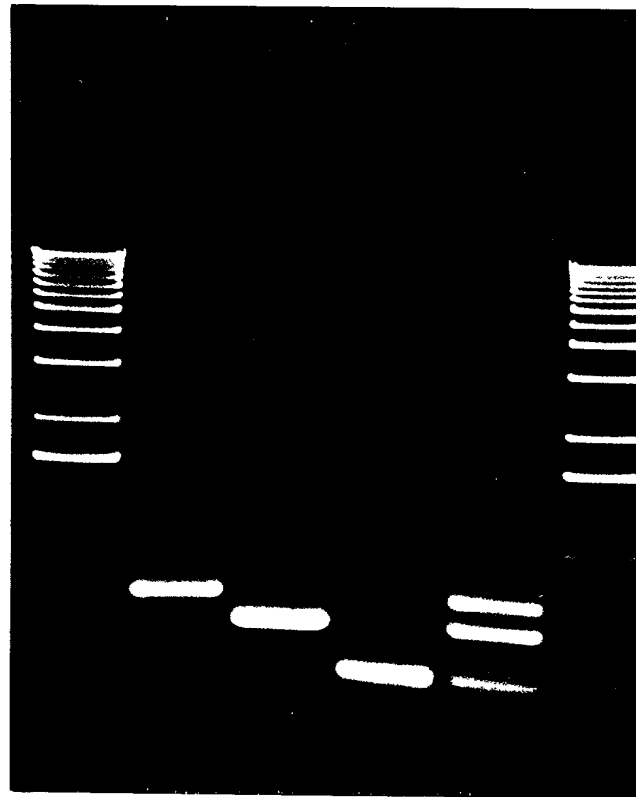


FIG.15

SM pVL1393 E M NP SM

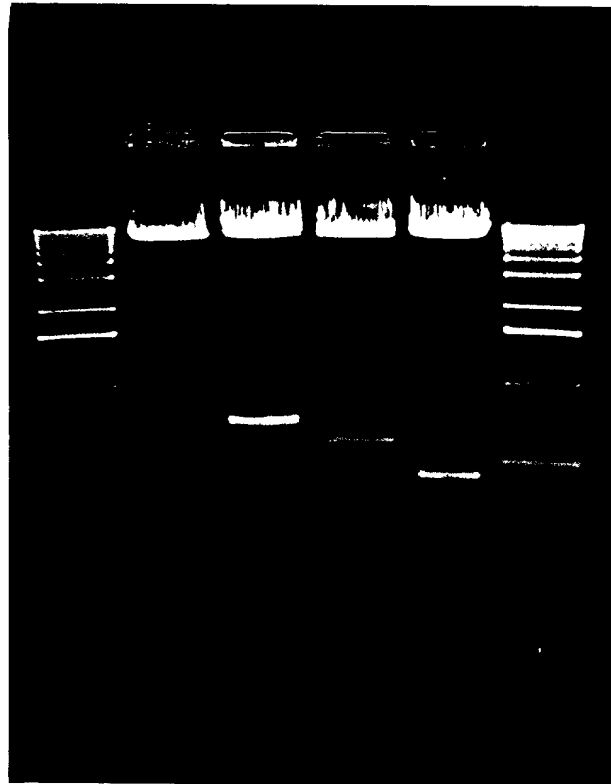


FIG.16

VR 2385	GTTTGTGCTTGGCTAGCGCGCAAGTACATTCTGGCCCTGCCCACCACGTTGAAAGTGGCCGAGGCTTCATCCGATTGGCGGCAAAATGATAACCAGCATT	398
ISU-1894	398
ISU-22	398
ISU-79	398
ISU-55T.....A.....	398
ISU-3927G.....	398
LV	A.....T.GC..T.....GCCA.....T.....A.....T.....TC.C...T.A..CT.A..GTC..G.....GA....A	395
VR 2385	TGTGCTCCGGGCTCCCGGCTCCACTACGGTCAACGGCACATTGGTGGCCGGGTAAAAAGCCTCGTGTGGGTGGCAGAAAAGCTGTTAAACAGGGAGTG	498
ISU-1894G.....	498
ISU-22T.....G.....	498
ISU-79G.....	498
ISU-55T.....G.....C.....	498
ISU-3927T.....G.G.....A.....G.....	498
LV	C.CT..GA.AAAG.....ACTA..AT.A..G.....TC.A..A..A..AC.TCGG.....C....C....A.CG.....GA.....	495
DRF 7 start		
+ 1> *** DRF 6 stop		
VR 2385	GTAACCTTGTAAATATGCCAAATAACACCGGCA-AGCAGCAGAGAGAAAGAA-----GGGGGATGGCCAGCCAGTCAATCAGCTGTG	582
ISU-1894C.....A.....-.....	582
ISU-22C.....A..T..-.....	582
ISU-79C.....A.....-.....	582
ISU-55A.....A.....-.....	582
ISU-3927T.....C.C..G...G.CGG...A.A..--..G...--..AAGTACAGCTCCGAT.....A.....A.....	582
LVT.....C.C..G...G.CGG...A.A..--..G...--..AAGTACAGCTCCGAT.....A.....A.....	591

FIG. 17B

VR 2385	CCAGATGCTGGGT--AA-GATCATCGCTCACC AAAACCAGTCCAGAGGCAAGGACCGGGAAGAAAAATAAGAAAGAAACCCGGAGAGCCCCATTTC	679
ISU-1894--..-.....G.....C.....T.....	679
ISU-22C--..-.....G....T.....	679
ISU-79--..-.....C..G.....T.....	679
ISU-55--..-.....G.....C.....	679
ISU-3927	...A.....--..-.....C..G.....T.....	679
LVT.....GC..T...A AGT.C..G.---G....-..-..CCT.G....-GCC..A.....G..T.....A.....T	679

VR 2385	CCTCTAGCGACTGAAGATGATGTCAGACATCACTTTACCCCTAGTGAGGTCATTGTTCTGTCGTCATCCAGACCGCCTTTAATCAAGGGCTGGGA	779
ISU-1894C.....G.....	779
ISU-22G.....	779
ISU-79G.....A..T.....	779
ISU-55C..T..G.....G.....A.....A.....	779
ISU-3927C.....C.....G.....T.....G.....	779
LV	..C..G..TG.....CA..C..G..C..C...AG.C...A..CTCCC.C..CT..CAA..G.....G..T..C.....A..A..	779

FIG. 17C

VR 2385	CTTGCACC-CTGTCAGATT	CAGGGAGGATAAGTTACACTGTGGAGTTAGTTTGCTACGCATCATAC	TGTGGCGCTGATCCGGTCACAGCATCACCC-	877
ISU-1894A.....T.....	877
ISU-22	877
ISU-79T.....	877
ISU-55T.....G.....G.....	877
ISU-3927C.....T.....T.....A.....G.....T.....G.....C.....	877
LV-.....GT.....G.....T.....TCCAGC.....A.....G.....C.....	TTCAG.....T.....TGC.....GGTTGC.....A.....G.....TTTA.....T.....G	878

VR 23 85	TCAG-CA-----TGA	*** ORF 7 stop	886
ISU-1894-.....		886
ISU-22-.....		886
ISU-79-.....		886
ISU-55-.....		886
ISU-3927-.....		886
LV	C.....T.....GGGTGCAAGT.A.	AAAAAAAAAAAA	898

FIG. 17D

VR 2385 DRF6 MESSLDFCHDSTAPQKVLLAFSITYTPVMYIALKVSRRLLGLLHLLVFLNCAFTFGYMTFVHFQSTNKVALTMGAWALLWGVSAIETWKFITSRCR 100
 ISU-1894 DRF6 , G.....I..... 100
 ISU-22 DRF6 , G.....I..... 100
 SIU-55 DRF6 , G.....I..... 100
 ISU-79 DRF6 , G.....Y.....M..... 100
 ISU-3927 DRF6 , G.....N.....I.....E...R..... 100
 LV DRF6 , G-G.....N.PI.A.,LV.....I.....S.....Y.....R...L.....FT,S..... 99
 PRRSV-10 DRF6 , G-G.....N.PI.A.,LV.....I.....S.....Y.....R...L.....FT,S..... 99
 LDV-C DRF2 , G-G,-E.,DQTSWY,-IFI.,L.....IA.,S.,F.,T.A.IVNIFI.,I.,CVS.V,LMYH,-SV.,T.I.,SL.,I.,V.,I.,TLVKIVDWLVI,... 96
 LDV-P DRF2 , G-G,-E.,DQTSWY,-I.I.,L.....IA.,S.,F.,T.A.IVNIFI.,I.,CVS.V,LMYH,-SV.,T.I.,SL.,I.,V.,I.,TLVKIVNMWVL,... 96

VR 2385 DRF6 LCLLGRKYILAPAHHVESAAGFHPAANDNH-----AFVRRPGSTTVNGTLVPGLKSLVLGGRKAVKQGVVNLVKY-AK 183
 ISU-1894 DRF6 ,.....-----,.....-.. 174
 ISU-22 DRF6 ,.....-----,.....-.. 174
 SIU-55 DRF6 ,.....-----,.....-.. 174
 ISU-79 DRF6 ,.....-----,.....-.. 174
 ISU-3927 DRF6 ,.....-----,.....R.....K.....-.. 174
 LV DRF6 ,..C...R.....L,S,S,SG,R-----,YA,K,L,S.....R.....KR.,R.....-GR 173
 PRRSV-10 DRF6 ,..C...R.....L,S,S,SG,R-----,YA,K,L,S.....R.....KR.,R.....-GR 173
 LDV-C DRF2 ,..F...S.....PS.,D-----TSDGRQSLTTSITI.,K...L...Q...DFQR.....K...SK.A...L...VS. 171
 LDV-P DRF2 ,..F...S.....PS.,D-----TSDGRQSLTTSITI.,K...L...Q...DFQR.....K...SK.A...L...VS. 171

FIG. 18A

VR 2385 DRF7	MPNNTGQQRKK-----GDGPVNQLCQMLGKIIAHQNSRGKGPCKKKNKKNPEKHPFLATEDDVRHHFTPSERQLCLSSIQTAFNQGAGTCTLS	100
ISU-1894 DRF7N.....-----Q.....	93
ISU-22 DRF7N.....-----Q.....	93
ISU-79 DRF7N.....-----Q.....	93
ISU-3927 DRF7N.....K.....-----Q.....	93
ISU-55 DRF7N.....K.....-----Q.....SG.....	93
VR2332 DRF7N.....TEE.....-----Q.....	93
LV DRF7--A.....N.SQ.,KKSTAPM,N.....L.,AM.KS.R.---QPR,GQA.,K.....A.....I.,L.QT.,S...Q.....AS.,	94
PRRSV-10 DRF7--A.....N.SQ.,KKSTAPM,N.....L.,AM.KS.R.---QPR,GQA.,K.....A.....I.,L.QT.,S...Q.....PS.,	94
LDV-C DRF1SQ.KK,GGQN,-----AN,---,N.LISALLRNAG,--N.,K.Q.K.,-Q,-L...M.GPS,L.,VM.,N.V.M.R.,LV.L.,G.Q.,V	85
LDV-P DRF1SQ.KK,SGQN,-----AN,---,N.LINALLRNAG,--N.,K.Q.K.,-Q,-L...M.GPS,L.,VM.,N.V.M.R.,LV.L.,G.Q.,V	85
EAV DRF7ASRRSRP,AASF-----RN,R--RRQPTSNDLLRMFG,-----MRVR,PPAQPTQAI,EPG,L.,DLNQQ.,ATLS,NV,RF,MI,H,SL,-A	83
~~~~~		
VR 2385 DRF7	DSGRISYTFVSLPTHHTVRLIRVTASP-----SA	134
ISU-1894 DRF7	.....	123
ISU-22 DRF7	.....	123
ISU-79 DRF7	.....	123
ISU-3927 DRF7	.....P,-----,	123
ISU-55 DRF7	.....	123
VR2332 DRF7	.....	123
LV DRF7	.....S.,KV,FQ.,M.,VA.,.....STSASQGAS	128
PRRSV-10 DRF7	.....S.,KV,FQ.,M.,VA.,.....STSASQGAS	128
LDV-C DRF1	.....G,NF.,S,M.,...A.,...NAS,NS-----,	115
LDV-P DRF1	.....G,NF.,S,M.,...A.,...NAS,NS-----,	115
EAV DRF7	.....A,GLT.,...SW-V.,KQIQ,KVAPP,G,-----	110
~~~~~		

FIG. 18B

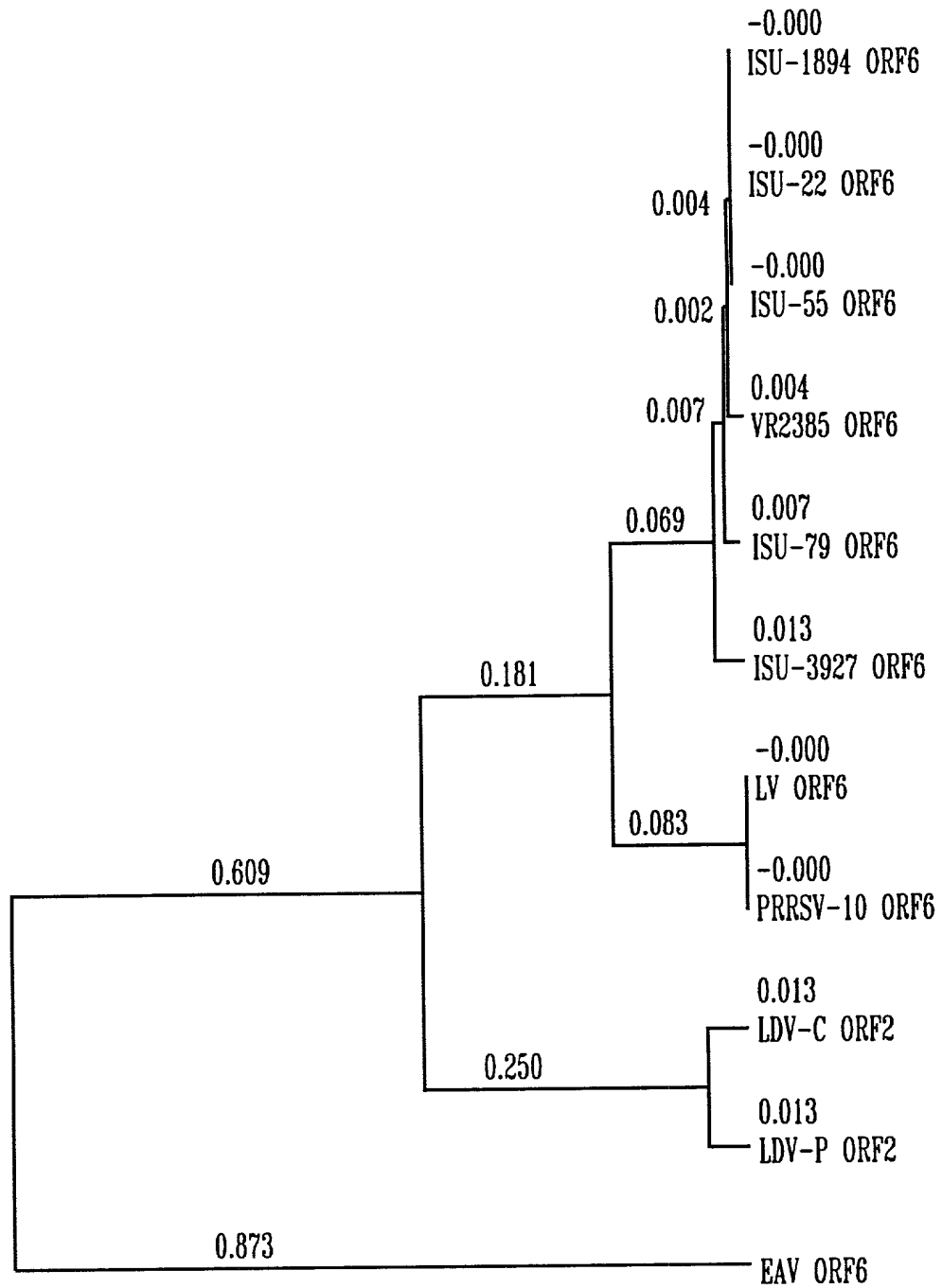


FIG. 19A

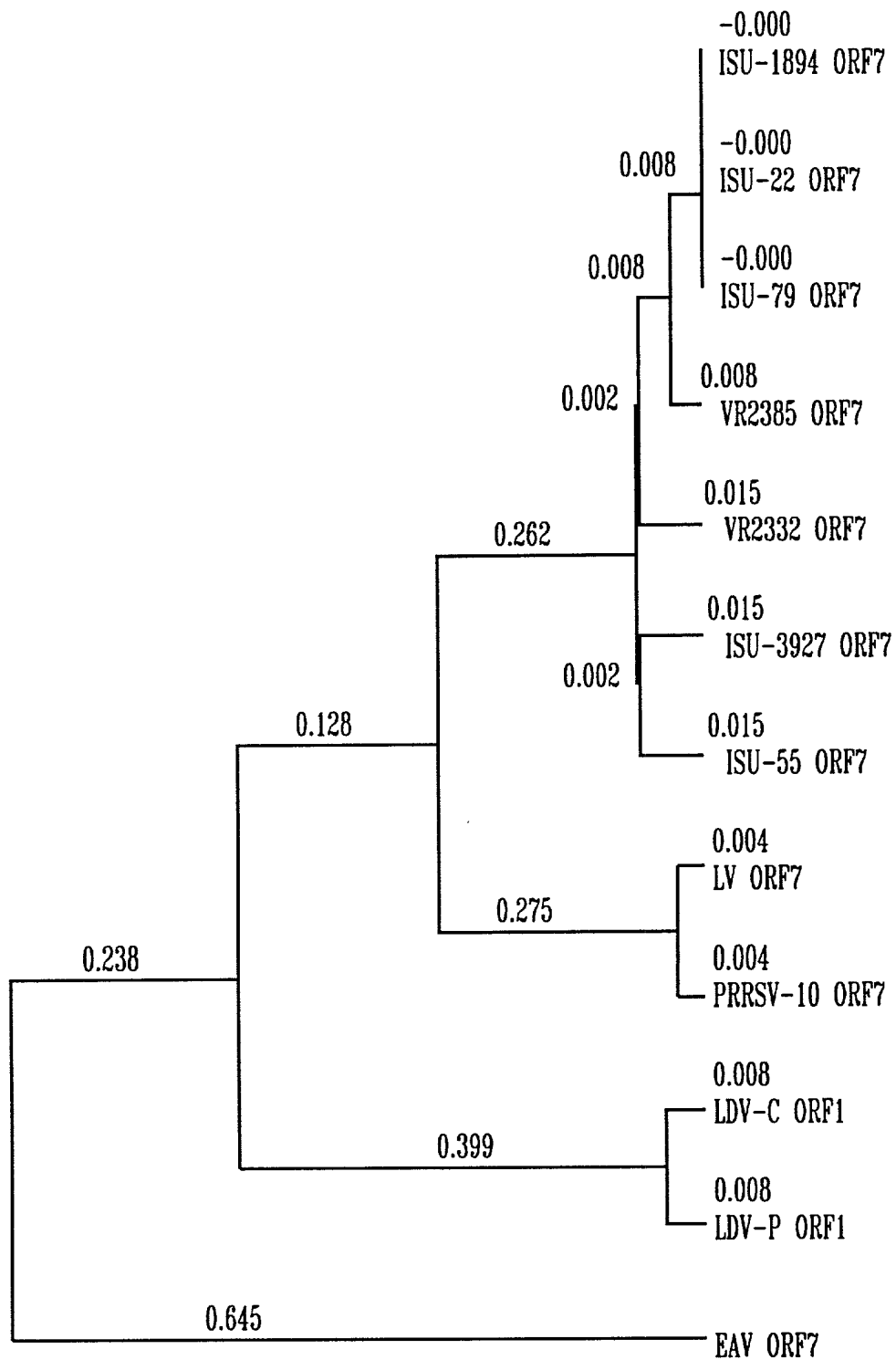


FIG. 19B

+ Start DRF2
 CCTGAATTGAGATGAGGATGCGGCTATGCAAGCCTTTTGACAAAATGGCCAACTTTTTGTGGATGCTTTCACGGAGTTCTTGGTGTCCATTGTTGAT 100
 ATCATTATATTTTTGGCCATTTGTTGGCTTCACCATCGCAGGTTGGCTGGTGGCTTTTGGCATCAGATTGGTTGGCTCCGGGATACTCCGTTGGCGGCC 200
 CTGCCATTCACTCTGAGCAATTACAGAAGATCCTATGAGGCCTTTCTCTCAGTGCCAGGTGGACATTCACCCTGGGGAACTAAACATCCTTTGGGGA 300
 TGCCTTGGCACCATAAGGTGTCAACCTGATTGATGAATGGTGTGCGTGAATGTACCGCATCATGGAAAAGCAGGACAGGCTGCCCTGGAAACAGGT 400
 AGTGAGCGAGGCTACGCTGTCTCGCATTAGTAGTTGGATGTGGTGGCTCATTTTCAGCATCTTGGCGCCATTGAAGCCGAGACCCTGTAATATATCTGGCC 500
 TCTCGGCTGCCCATGCTACACCACCTGCGCATGACAGGCTCAAAATGTAACCATAGTGTATAATAGTACTTTGAATCAGGTGTTTGGCTGTTTCCCAACCC 600
 CTGGTCCCGGCCAAGCTTCATGATTTCCAGCAATGGCTAATAGCTGTACATTCCTCTATATTTTCCCTGTGTGCAGCTTCTTGTACTCTTTTGTGT 700
 + Start DRF3
 GCTGTGGTTGCGGGTTCCAATGCTACGTACTGTTTTTGGTTTCCGCTGGTAGGGGCAATTTTCTTTCGAACTCAGGTTGAATTACACGGTGTGGCCG 800
 CTTGCCCTACCCGGCAAGCAGCCGCGAGAGGCTACGAACCCGGCAGGTCCCTTTGGTGCAGGATAGGGCATGATGATGTGGGAGGACGATCATGATGA 900
 ACTAGGGTTTGTGTGGCTCTCGGCTCTCCAGCGAAGGCCACTTGACCAGTGCTTACGCCGTGGTGGCGTCCCTGTCCCTTCAGCTATACGGGCCAGTTT 1000
 CATCCCGAGATATTCGGGATAGGGAATGTGAGTCGAGTCTATGTTGACATCAGCACCAATTCATTTGGCGTGTTCATGATGGGAGAACACCACCTTGC 1100

*** Stop DRF2

FIG. 20A

+ Start DRF4
 CCCACCATGACAACATTTACAGCCGTGCTTCAGACCTATTACCAGCATCAGGTCGACGGGGGCAATTGGTTACCTAGAATGGTGCGCTTCCTTCTTTC 1200
 CTCCTGGTTGGTTTTAAATGTCCTCTGGTTCTCAGGGCTTCGGCTGCAAGCCATGTTTCAGTTCGAGTCCTTCAGACATCAAGACCACACACCACCGCAG 1300
 *** Stop DRF3
 CGGCAGGCTTTGCTGTCTCCAAGACATCAGTTGCCTTAGGCATCGCAACTCGGCCCTCTGAGGCGATTGCAAAAGTCCCTCAGTGGCGCAGCGGATAGG 1400
 GACACCCGTGTATACACTGTCACAGCCCAATGTTACCGATGAGAATTATTGGCATCCCTCIGATCTTCATGCTTTCCTTGGCTTTTCATGCTTCT 1500
 GAGATGAGTGAAAAGGGATTTAAGGTGGTATTGGCAATGTGTGAGGCATCGTGGCAGTGTGGGTCAACTTACCAGTTACGTCCAACATGTCAAGGAAT 1600
 TTACCCAACGTTCCCTTGGTAGTTGACCATGTGCGGGCTGCTCCATTTTCATGACGCCCGAGACCATGAGGTGGGCAACTGTTTTAGCCIGCTTTTTTACCAT 1700
 *** Stop DRF4 + Start DRF5
 TCTGTTGGCAATTTGAATGTTAAGTATGTTGGGGAAATGCTTGACCGCGGGCTGTGTGCTCGCAATTGCTTTTTTATGGTGTATCGTGCCGCTTGTT 1799

FIG. 20B

Consensus	ATGMAATGGGGTCWMTGYRRAGCCTTTTGAYAAAAATYRGCCARCTKTTYGTGGAYGCTTCACKGAGTTCYTKGKWSYRTKGTGATATYRYATWTT	100
VR2385 DRF2	...A...TA...CAA...C...TG...A...T...T...G...GTCCA...T...CATT...A...	100
LV DRF2	...C...AC...TGG...-----T...CA...G...C...C...T...TAGTG...G...TGC...T...	91
Consensus	YYTKGCCATWYTGTTGGSTTACCRTCCAGGWTGGYTRSTGGTCTTYKYMTCAGAKTGTTGTCCGGGMTWCTCCGTCGGCGCYCTGCCATTAC	200
VR2385 DRF2	TT...G...TT...C...A...T...C...GG...TGCA...T...A...G...C...	200
LV DRF2	CC...T...AC...G...G...A...T...AC...CTTC...G...C...T...T...	191
Consensus	TCTSMSSAAYTAYMGAAGRTCCATGARGSCCTKYTSYCYMASTGCMRRSYGGAYAKTCCACAMTKKGSARYAARCAAYCCWTTGGGKATGYTTGGCA	300
VR2385 DRF2	...GAGC...T...CA...A...G...C...TC...CT...G...CAGGT...C...T...-C...GG...G...ACT...A...T...T...G...C...	299
LV DRF2	...CCCG...C...TC...G...A...G...GT...GC...CA...C...AGACC...T-G...A...TT...C...GTC...G...C...A...T...T...	290
Consensus	CCATRMGAGTKTCMMMYCTGATTGATGARATGGTSTCKCGTCGMATKTACCRSAYCATGGAAWKCAGGWCARGCKGCTGGAAARCAGGTGTRGTRGYGA	400
VR2385 DRF2	...AA...G...AAC...C...A...G...G...A...G...GC...T...A...AG...A...G...T...A...A...A...GA...C...	398
LV DRF2	...GC...T...CCA...T...G...C...T...C...T...AG...C...T...T...T...A...G...G...G...G...T...G...T...	389
Consensus	GGCYACGCTSTCWCMAKYWGTCAGGKYTSGATRTGTRGTRKCTCATTTTCARCACTKGGCGCMRTKGARGCSGAKWCYTGYNMTWTCTSRSCCTCWGRC	500
VR2385 DRF2	...T...G...T...C...TTA...-...-...TT...G...G...G...G...T...T...G...T...CA...T...A...C...GA...C...TAAA...A...GGC...T...G...	496
LV DRF2	...C...-...C...A...A...GCT...GC...C...A...A...TA...C...A...C...G...AG...G...G...T...T...T...CCGC...T...CAG...A...A...	487

FIG. 21A

[illegible]

FIG. 21A. 1

Consensus	ATGGCTMATMRSTGTRCAYKCYTCYATWTTTTCCCTCTGTGCKWKCWTCTKKTACYYTKTYRTWTGCTGTGGYTKCGRRTTCCARYKCTACGYWMTGTT	100
LV DRF3C..CAG...G..CG.T..C..T.....G..TT.A...GT...CT..G..CA.A....T...C.T..AA....GCT.....CTA....	100
VR2385 DRF3A..AGC...A..TT.C..T..A.....T..AG.T...TG...TC.T...TG.T....G...T..G..GG....ATG.....TAC....	100
Consensus	TTTGGTTTCCRYTGYYMRSGGCAAYWWTCTTCGARCTSACSRTSAAYTACACSRTRTGCWYGCCYTGYYAYCCMGKCAAGRGCTCGCMRARGSCT	200
LV DRF3AT...CCCAC.....CACAA..A....G..G..CA.C..C....CA.A..AT...C..TTCT...A.T....G.....CA.A.G..	200
VR2385 DRF3GC...TTAGG.....TTTT..T.....A..C..GG.G..T.....GG.G..CC...T..CCTC...C.G....A..-...AG.G.C..	199
Consensus	ACGARCCCGGYMGKWMCMTKTGTGTCARRATAGGGCATGAYMGRGTGTGRGGAGSRYGAYCATGATGARYTAGKKWWTGTCSRTSCCGTCYGGSYWCKMCA	300
LV DRF3	-...G....TC.TAA.A.G.....AA.....CA.G...A....CGT..C.....GT..-..TTAA....CA.C....C..GTA.GA..	298
VR2385 DRF3A....CA.GTC.C.T.....GG.....TC.A...G....GAC..T.....AC...GGTT...-GG.G....T..CCT.TC..	298
Consensus	sRCGAMKSMMACTTGACSRGTKMTTAYGCTGGYTGCGKTYYYTGCTTYWCTAYRCGGCCARTTCCATCCSGAGWTRTTCGGGATAGGGAATGTGWS	400
LV DRF3	A.--CTCAA.....-GG..TA...T..T...C...T.TTT.....TTC...CG.....A.....G...T.G.....TC	395
VR2385 DRF3	G...AGGCC.....CA..GC...C..C..T...G.CCC.....CAG..TA.....G.....C...A.A.....AG	398
Consensus	KCGMGTCTWYGTGACAWSMRRACCACTTCATTGTGYGYGWKCATGATGRCASAAAYWCMACCKTRYCYMMSRWSACAATYTCMGCMKTRYVTSMG	500
LV DRF3	G..C....TC..G....AGCGA.....G.....T..C..AG.....A..C..TT.A...G.AT.TAC.GGAC.....C..C..AT.ATA.GC.	495
VR2385 DRF3	T..A....AT..T....TCAAG.....A.....C..T.TT.....G..G..CA.C...T.GC.CCA.CATG.....T..A..CG.GCT.CA.	498

FIG. 21B

Consensus	RCMTATTACCASCAYCARRTMGACGGGGCAATTGGTTCAYYTRGAATGGSTGGCKCMYCTCTTTCYTCYTGGYTGGTKYTMAYRTMTCWTGGTTTC	600
LV DRF3	G. A. C. . C. . AA. A. C. . TT. G. C. G. . AC. T. . C. C. GC. C. CA. A.	595
VR2385 DRF3	A. C. G. . T. . GG. C. T. . CC. A. G. T. . CT. C. . T. T. . A. TG. C. . T.	598
Consensus	TSAGGCGTTCGCCTGYAAGCCMTGTTTCWSKWCGMRCTCTWTCAGAYATYRAGACCAACACSACCGCRGCKGCMGGYTTYRYKGTCCCTYCARGACATCART	700
LV DRF3	. G. T. C. TCGA. . CA. A. T. . TG. G. G. . T. . C. . T. CATG. T. . G. A.	695
VR2385 DRF3	. C. C. A. AGTT. . AG. T. C. . CA. C. A. . G. . A. . C. TGCT. C. . A. G.	698
Consensus	TGYYTYMGRCMTCACGGSRWCTCRGCAGCKCAWGAGRMRAITTCCTTCGSAAGTCGYCYCARTIGYCGYGAMGSCGWYRGTACTCCCCAGTACATCACGA	800
LV DRF3	. . TT. CC. A. C. GGT. A. G. A. AAA. G. T. . C. . A. . T. A. . C. TCG.	795
VR2385 DRF3	. . CC. TA. G. A. CAA. G. T. . -T. GCCG. C. -C. T. . G. . C. . C. . -C. . G. . ATA.	765
Consensus	TAA	803
LV DRF3	. . .	798
VR2385 DRF3	---	765

FIG. 21B.1

	Consensus	ATGGSTGGCKCCMYTC	TTTTCYTCYTG	GGTKY	TMAAYRT	MCWTG	TTTCT	SAGCG	TTG	TTCTC	SKVCG	MRCTCT	TWTCAGAYA	100
VR2385	QRF4G....T...CT.....C...T...T....	TT.A.	TG.C.	T.....	C.....	C.....	A.....	AGTT..	AG...T.....	C.	100	
LV	QRF4C....G..AC.....	T...C...C....	GC.C.	CA.A.	A.....	G.....	T.....	C.....	TCGA..	CA...A.....	T.	100	

Consensus	TYRAGACCAACAC	SACCGCRGCKGCMGG	YTYRYKGTCTCTY	CARGACATCAT	TTGGYYTYMGRCMT	CACGSRWCTCRG	CAGCKCAWAG	MRATTTTCCTT	200
VR2385	CAC.....	A..G..A..C..TGCT.....	C..A.....G..CC..TA..G..A..---	CAA..G..--..T..	..GCG..	-----	..	189
LV	ORF4	..TG.....	..G.....G..T..C..T..CATG.....	T..G.....A..TT..CC..A..C.....	GgT...A.....G..A..AAA.....	200

Consensus	CGSAAAGTCGYCYCARTGTCGYRMGCSRTMGGKACWCCCSWGTAYATCACKRTMACRCGYAAVGTACCGAYGARWMTAYTTGAYYMWCKCKGAYCTK	300
VR2385 DRF4	..C.....-C.T..G..C..CACG..GA.A..G..A...GT...T....TG.C..A..C..T..T....T..GAAT..T...C..TTC.T.T..T..T	288
LV DRF 4	..G.....T.C..A..T..TGAA..CG.C..T..T..CA...C.....GA.A..G..T..C..G.....C..ATCA..C...T.CAA.G.G..C..G	300

	Consensus	400
VR2385	QRF4	388
LV	QRF4	400

Consensus	AYTTCACMRRTTAYGTSSMMCATGTCAAGGAATTACCCCAACATACCCAGCAGYATCAYYTTGGTARTTTGAYCAYRTKGGYTGCTSCATTTTCMTGACRCC	500
VR2385	.C.....CAG...C..CCAA.....T-..-CT.....G....C...TG.G...C....C.....A....G..	476
IV	.T.....AGA...T...GGCC.....C....TC.....A....T..CA.T...T...G.....C....A..	491

Consensus	MMKMKRCMATGAGGTGGGGC W ACWRY Y WTWGCYTGTYKTTYRCCATTCTSTTGGCAATWTGA	561
VR2385 DRF4	CGAGA, C, A, TGTT, A, C, . . . C, T, TA, G, T, . .	537
LV DRF4	ATCTG, A, T, AACCA, T, T, . . . T, G, CG, C, A, . .	552

FIG. 21C

Consensus	M. WG. C., K., L., W., L., SL., P. CL. SPSQ. G. WSF. S. WFAPR. SVRALPFTL. NYRRSYE., L., C., D. P., KH	100
LV DRF2.	. Q., H. GV. SASCSWTPS. SSLLV. LI-----, PF., Y., G., D. Y., F. E., F., P., GL. PN. RP. V. QFAV.,	90
VR2385 DRF2.	. K., L., ----AFLTK. AN-FL. MLSSSWCP. LI., YFW. F., A., V. W., A. D., Y., S., AF. SQ. QV. I. TWGT.,	93
Consensus	PLGM. WH., VS. LIDEMVSRR. Y., ME., GGAANKQVV. EATL., S. LD. V. HFQHLLAA. EA., C., L. SRL. ML., L., NV., YN. TL., V.,	200
LV DRF2. F., MR., H., I. QT., HS., G., TKL. G., I. T., V., DS. RF. S., V., KN. AV--G., SLQ., T., DR. ELI	188
VR2385 DRF2. L., HK., T., M. RI., KA., S., SRI. S., V. A., I., ET. KY. A., P., HH. RMTGS., TIV., S., NQ. FAV	193
Consensus	FPTPG. RPKL. DF. QWLI. VH. SIFSSVA. S. TLF. VLWLR. P. LR. VFGF. W., A.,	264
LV DRF2. T., T., R., S., A., S. V., I., I. A., Y., H. PT., ---THSS	249
VR2385 DRF2. S., H., Q., A., S., A. C., V., V. M., T., R. LG. IFLSNSR-	257

FIG. 22A

Consensus	MA, C, ..., FLC, ..., Y, ..., A, ..., S, T, CFWFPL, GN, SFELT, NYT, C, PC, T, QAA, ..., EPGR, WC, IGHDRC, E, DHDEL, ..., PSG, ...	100
LV DRF3,	.. HQ, ARHF, ..., GFIC, LVHS, LASN, SS, L, ..., AH, T, ..., I, I, M, S, S, ..., RQRL, ..., NM, K, ..., E, R, ..., LMSI, ..., YDN	100
VR2385 DRF3,	.. NS, TFLYI, ..., CSFL, SFCC, VWAG, NA, Y, ..., VR, F, ..., V, V, P, L, R, ..., AEAY, ..., SL, R, ..., G, D, ..., GFVV, ..., LSS	100
Consensus	... L, ... YAWLA, LSFSY, AQFHPE, FGIGNSV, VD, ..., HQFICA, HDG, N, T, ..., NISA, ..., YY, HQ, DGGNWFHLEW, RP, FSSWLVLN, SWFL	200
LV DRF3,	L-K, EGY, ..., F, ..., A, ..., L, ..., F, KR, ..., E, H, S, VSTGH, ..., LYAA, H, I, ..., L, L, ..., I, ...	199
VR2385 DRF3,	EGH, TSA, ..., S, ..., T, ..., I, ..., Y, IK, ..., V, Q, T, LPHHD, ..., VLQT, Q, V, ..., V, F, ..., V, ...	200
Consensus	RRSP, S, VS, R, Q, RPT, P, ..., S, TS, ..., L, ..., R, F, ..., K, S, ...	266
LV DRF3,	..., V, P, R, IY, IL, ..., R, RLPVSW, FR, ..., IVSD, TGSQQRK, K, PSES RPNV, P, VLPSTSR	265
VR2385 DRF3,	..., A, H, V, VF, TS, ..., P, QRQALL, SK, V--A, GIATRPL, R, A-----, -LSAARR-	255

FIG. 22B

Consensus	M, A, LF, L, G, ..., VS, AFACKPCFS, ..., LSDI, TTTAAAGF, VLQDI, C, R, ..., A, E, I, ..., K, QCR, A, GTP, YIT, TANVTDE, YL, ..., DL	100
LV DRF4,	A, AT, F, A, AQHIM, E, ..., TH, ..., E, ..., M, ..., N, F, PHGVSA, Q, K, SFG, SS, ..., E, V, ..., Q, I, ..., S, YNA, ...	100
VR2385 DRF4,	G, SL, L, V, FKCLL, Q, ..., SS, K, ..., A, ..., S, L, HR--NS, S, A, R--, VP, T, I, V, ..., V, ..., N, HSS, ...	96
Consensus	LMLS, CLFYASEMSEKGFKV, FGNVSG, V, CVNFT, YV, HV, ..., TQ, ..., V, ..., RLLHF, TP, MRWAT, ACLF, ILLAI, ...	184
LV DRF4,	..., A, ..., V, SA, ..., D, A, A, TQH, QHHL, IDHI, ..., L, SA, ..., TI, ..., A, ...	183
VR2385 DRF4,	..., S, ..., V, ..., I, AV, ..., S, Q, KEF, RSLV, DH-V, ..., M, ET, ..., VL, ..., T, ...	179

FIG. 22C

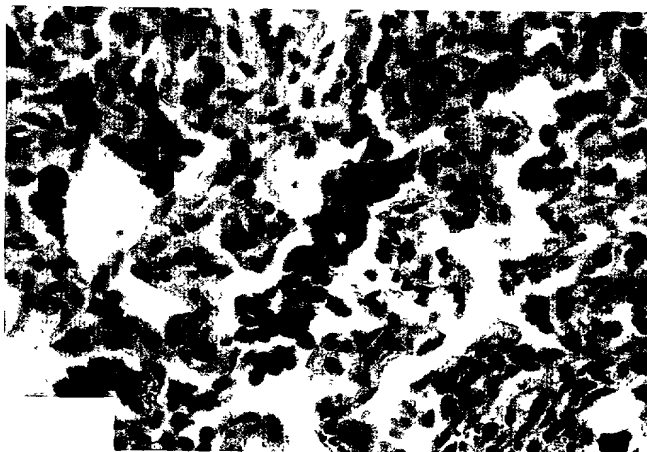


FIG.23

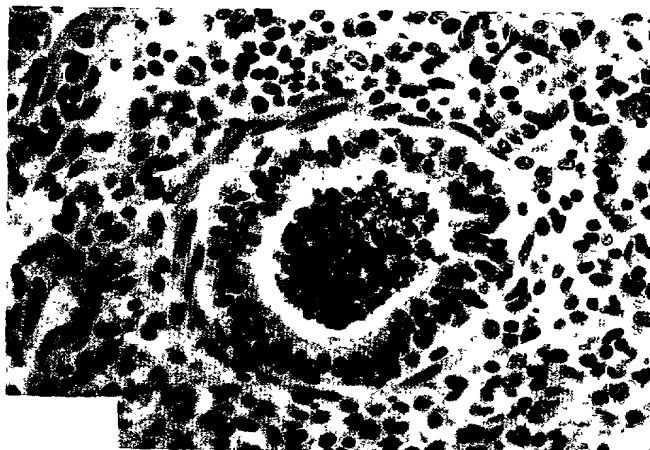


FIG.24

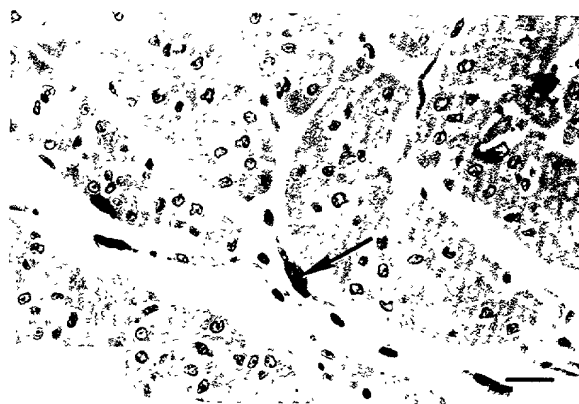


FIG.25

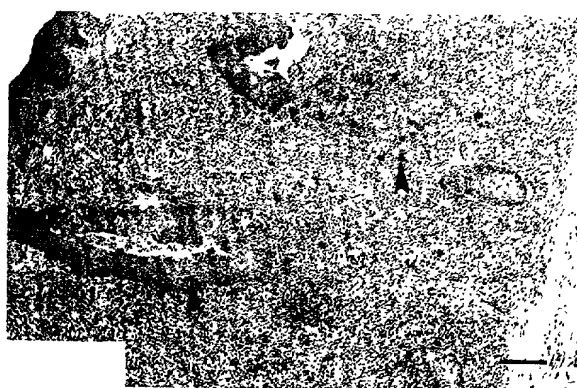


FIG.26

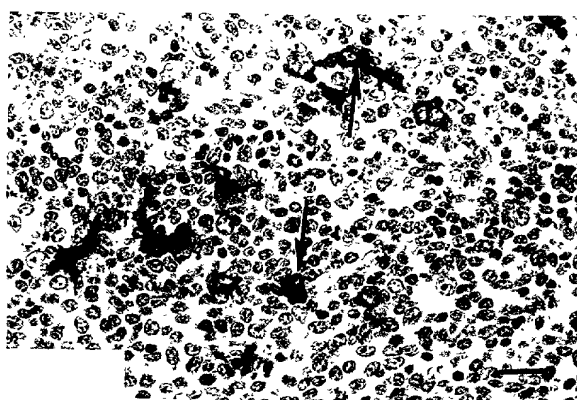


FIG.27



FIG. 28A



FIG. 28B



FIG. 28C

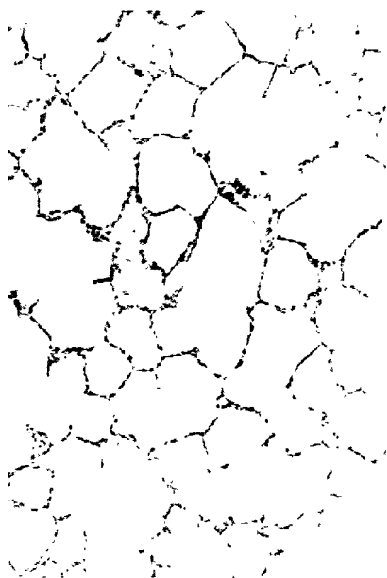


FIG. 29A



FIG. 29B



FIG. 29C

22 55 79 1894 3927



1

1

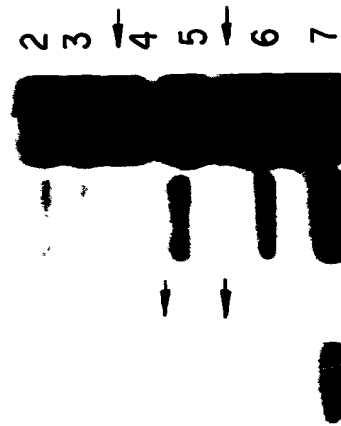


FIG.30A

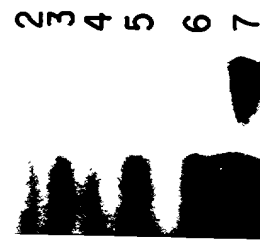


FIG.30B